



SEQUENCE LISTING

<110> KOLTERMAN, ORVILLE G.

YOUNG, ANDREW A.

RINK, TIMOTHY J.

BROWN, KATHLEEN ANN KEATING

<120> METHODS FOR REGULATING GASTROINTESTINAL MOTILITY

<130> 18528.642

<140> 10/643,681

<141> 2003-08-18

<150> 09/576,062

<151> 2000-05-22

<150> 08/302,069

<151> 1994-09-07

<150> 08/118,381

<151> 1993-09-07

<160> 31

<170> PatentIn Ver. 3.3

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>

<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>

<221> MOD_RES

<222> (37)

<223> amidated Tyr (Tyrosinamide)

<400> 1

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

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peptide construct

<220>
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<222> (24)
<223> amidated Tyr (Tyrosinamide)

<400> 2
Leu Gly Arg Leu Ser Gln Glu Leu His Arg Leu Gln Thr Tyr Pro Arg
1 5 10 15
Thr Asn Thr Gly Ser Asn Thr Tyr
20

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peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
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<223> amidated Tyr (Tyrosinamide)

<400> 3
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15
Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
35

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peptide construct

<220>

<223> Disulfide bridge between the Cys residues at positions 1 and 6

<220>

<221> MOD_RES

<222> (36)

<223> amidated Tyr (Tyrosinamide)

<400> 4

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
1 5 10 15

His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val Gly
20 25 30

Ser Asn Thr Tyr
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<223> Disulfide bridge between the Cys residues at positions 2 and 7

<220>

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<222> (37)

<223> amidated Tyr (Tyrosinamide)

<400> 5

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Pro Ser Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
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<222> (36)

<223> amidated Tyr (Tyrosinamide)

<400> 6

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
1 5 10 15

Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val Gly
20 25 30

Ser Asn Thr Tyr
35

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<223> amidated Tyr (Tyrosinamide)

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Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Val His Ser Ser Asn Asn Phe Gly Pro Val Leu Pro Pro Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
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 <223> amidated Tyr (Tyrosinamide)

 <400> 8
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
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 Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val
 20 25 30

 Gly Ser Asn Thr Tyr
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 <400> 9
 Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
 1 5 10 15
 Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val Gly
 20 25 30

 Ser Asn Thr Tyr
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 Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
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 His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val Gly
 20 25 30

 Ser Asn Thr Tyr
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 <223> amidated Tyr (Tyrosinamide)

 <400> 11
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
 1 5 10 15
 Val His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Pro Thr Asn Val
 20 25 30

 Gly Ser Asn Thr Tyr
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<223> amidated Tyr (Tyrosinamide)

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Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Val His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
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20 25 30

Ser Asn Thr Tyr
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 Val Arg Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val
 20 25 30

 Gly Ser Asn Thr Tyr
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 <222> (37)
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 <400> 15
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 1 5 10 15
 Val Arg Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Pro Thr Asn Val
 20 25 30

 Gly Ser Asn Thr Tyr
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20 25 30
Gly Ser Asn Thr Tyr
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<222> (37)
<223> amidated Tyr (Tyrosinamide)

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Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
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Ile His Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Pro Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
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positions 2 and 7

<220>
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<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 18
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
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Ile His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
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<220>
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Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Ile
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His Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Pro Thr Asn Val Gly
20 25 30
Ser Asn Thr Tyr
35

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 Ile Arg Ser Ser Asn Asn Leu Gly Ala Ile Leu Ser Ser Thr Asn Val
 20 25 30

 Gly Ser Asn Thr Tyr
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 20 25 30

 Gly Ser Asn Thr Tyr
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1 5 10 15

Ile Arg Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Pro Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

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positions 2 and 7

<220>
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<400> 23
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
1 5 10 15

Val His Ser Ser His Asn Leu Gly Ala Ala Leu Leu Pro Thr Asp Val
20 25 30

Gly Ser Asn Thr Tyr

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<220>
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<400> 24
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
 1 5 10 15

Val His Ser Ser His Asn Leu Gly Ala Ala Leu Ser Pro Thr Asp Val
 20 25 30

Gly Ser Asn Thr Tyr
 35

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<220>
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His Ser Ser His Asn Leu Gly Ala Ala Leu Pro Ser Thr Asp Val Gly
 20 25 30

Ser Asn Thr Tyr
35

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positions 2 and 7

<220>
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Val Arg Ser Ser His Asn Leu Gly Ala Ala Leu Ser Pro Thr Asp Val
20 25 30

Gly Ser Asn Thr Tyr
35

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peptide construct

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positions 2 and 7

<220>
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<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 27
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
1 5 10 15

Val Arg Ser Ser His Asn Leu Gly Ala Ile Leu Pro Pro Thr Asp Val
20 25 30

Gly Ser Asn Thr Tyr
35

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positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 28
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
1 5 10 15

Val Arg Ser Ser His Asn Leu Gly Pro Ala Leu Pro Pro Thr Asp Val
20 25 30

Gly Ser Asn Thr Tyr
35

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<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
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<222> (25)
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<400> 29
Val Leu Gly Lys Leu Ser Gln Glu Leu His Lys Leu Gln Thr Tyr Pro
1 5 10 15

Arg Thr Asn Thr Gly Ser Asn Thr Tyr
20 25

<210> 30

<211> 25
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 peptide construct

 <220>
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 <222> (25)
 <223> amidated Pro (Prolinamide)

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 1 5 10 15
 Arg Thr Asn Thr Gly Ser Gly Thr Pro
 20 25

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 Lys

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 <223> Variable amino acid

 <220>
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 <223> Variable amino acid

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 <222> (13)
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 <222> (17)
 <223> Val, Leu, or Ile

 <220>

<221> MOD_RES
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 <223> His or Arg

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 <223> Ser or Thr

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 <223> Ser, Thr, Gln, or Asn

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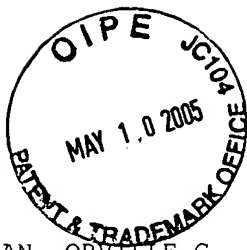
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 <222> (29)
 <223> Ser, Pro, or Thr

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 1 5 10 15
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 20 25 30
 Gly Ser Asn Thr Tyr



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<140> 10/643,681

<141> 2003-08-18

<150> 09/576,062

<151> 2000-05-22

<150> 08/302,069

<151> 1994-09-07

<150> 08/118,381

<151> 1993-09-07

<160> 31

<170> PatentIn Ver. 3.3

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peptide construct

<220>

<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>

<221> MOD RES

<222> (37)

<223> amidated Tyr (Tyrosinamide)

<400> 1

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

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 peptide construct

 <220>
 <221> MOD_RES
 <222> (24)
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 <400> 2
 Leu Gly Arg Leu Ser Gln Glu Leu His Arg Leu Gln Thr Tyr Pro Arg
 1 5 10 15

 Thr Asn Thr Gly Ser Asn Thr Tyr
 20

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<220>
 <223> Disulfide bridge between the Cys residues at
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 <222> (37)
 <223> amidated Tyr (Tyrosinamide)

<400> 3
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
 1 5 10 15

 Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val
 20 25 30

 Gly Ser Asn Thr Tyr
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 positions 1 and 6

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<400> 4
Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
1 5 10 15
His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val Gly
20 25 30
Ser Asn Thr Tyr
35

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positions 2 and 7

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<400> 5
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15
Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Pro Ser Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
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 Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
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 Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val Gly
 20 25 30
 Ser Asn Thr Tyr
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 <222> (37)
 <223> amidated Tyr (Tyrosinamide)

<400> 7
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
 1 5 10 15
 Val His Ser Ser Asn Asn Phe Gly Pro Val Leu Pro Pro Thr Asn Val
 20 25 30
 Gly Ser Asn Thr Tyr
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 <223> amidated Tyr (Tyrosinamide)

<400> 8
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
 1 5 10 15

Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
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<222> (36)
<223> amidated Tyr (Tyrosinamide)

<400> 9
Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
1 5 10 15

Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val Gly
20 25 30

Ser Asn Thr Tyr
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positions 1 and 6

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<222> (36)
<223> amidated Tyr (Tyrosinamide)

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Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
1 5 10 15

His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val Gly
20 25 30

Ser Asn Thr Tyr
35

<210> 11
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 11
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Val His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Pro Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

<210> 12
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 12
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Val His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

<210> 13
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 1 and 6

<220>
<221> MOD_RES
<222> (36)
<223> amidated Tyr (Tyrosinamide)

<400> 13
Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
1 5 10 15
His Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val Gly
20 25 30
Ser Asn Thr Tyr
35

<210> 14
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 14
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15
Val Arg Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Ser Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
35

<210> 15

<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 15
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15
Val Arg Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Pro Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
35

<210> 16
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 16
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15
Val Arg Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Ser Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
35

<210> 17
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 17
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15
Ile His Ser Ser Asn Asn Leu Gly Pro Ile Leu Pro Pro Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
35

<210> 18
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 18
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15
Ile His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
35

<210> 19
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

peptide construct

<220>

<223> Disulfide bridge between the Cys residues at positions 1 and 6

<220>

<221> MOD_RES

<222> (36)

<223> amidated Tyr (Tyrosinamide)

<400> 19

Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu	Ile
1				5				10					15		

His	Ser	Ser	Asn	Asn	Leu	Gly	Pro	Ile	Leu	Pro	Pro	Thr	Asn	Val	Gly
			20					25					30		

Ser	Asn	Thr	Tyr
			35

<210> 20

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide construct

<220>

<223> Disulfide bridge between the Cys residues at positions 2 and 7

<220>

<221> MOD_RES

<222> (37)

<223> amidated Tyr (Tyrosinamide)

<400> 20

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe	Leu
1				5					10					15	

Ile	Arg	Ser	Ser	Asn	Asn	Leu	Gly	Ala	Ile	Leu	Ser	Ser	Thr	Asn	Val
			20					25					30		

Gly	Ser	Asn	Thr	Tyr
				35

<210> 21

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide construct

<220>

<223> Disulfide bridge between the Cys residues at positions 2 and 7

<220>

<221> MOD_RES

<222> (37)

<223> amidated Tyr (Tyrosinamide)

<400> 21

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Ile Arg Ser Ser Asn Asn Leu Gly Ala Val Leu Ser Pro Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

<210> 22

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide construct

<220>

<223> Disulfide bridge between the Cys residues at positions 2 and 7

<220>

<221> MOD_RES

<222> (37)

<223> amidated Tyr (Tyrosinamide)

<400> 22

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15

Ile Arg Ser Ser Asn Asn Leu Gly Pro Val Leu Pro Pro Thr Asn Val
20 25 30

Gly Ser Asn Thr Tyr
35

<210> 23

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide construct

<220>

<223> Disulfide bridge between the Cys residues at positions 2 and 7

<220>
 <221> MOD_RES
 <222> (37)
 <223> amidated Tyr (Tyrosinamide)

 <400> 23
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
 1 5 10 15
 Val His Ser Ser His Asn Leu Gly Ala Ala Leu Leu Pro Thr Asp Val
 20 25 30
 Gly Ser Asn Thr Tyr
 35

<210> 24
 <211> 37
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide construct

<220>
 <223> Disulfide bridge between the Cys residues at positions 2 and 7

<220>
 <221> MOD_RES
 <222> (37)
 <223> amidated Tyr (Tyrosinamide)

<400> 24
 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
 1 5 10 15
 Val His Ser Ser His Asn Leu Gly Ala Ala Leu Ser Pro Thr Asp Val
 20 25 30
 Gly Ser Asn Thr Tyr
 35

<210> 25
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide construct

<220>
 <223> Disulfide bridge between the Cys residues at positions 1 and 6

<220>
 <221> MOD_RES
 <222> (36)

<223> amidated Tyr (Tyrosinamide)

<400> 25

Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu Val
1 5 10 15

His Ser Ser His Asn Leu Gly Ala Ala Leu Pro Ser Thr Asp Val Gly
20 25 30

Ser Asn Thr Tyr
35

<210> 26

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>

<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>

<221> MOD_RES

<222> (37)

<223> amidated Tyr (Tyrosinamide)

<400> 26

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
1 5 10 15

Val Arg Ser Ser His Asn Leu Gly Ala Ala Leu Ser Pro Thr Asp Val
20 25 30

Gly Ser Asn Thr Tyr
35

<210> 27

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>

<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>

<221> MOD_RES

<222> (37)

<223> amidated Tyr (Tyrosinamide)

<400> 27

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
1 5 10 15

Val Arg Ser Ser His Asn Leu Gly Ala Ile Leu Pro Pro Thr Asp Val
20 25 30

Gly Ser Asn Thr Tyr
35

<210> 28
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<223> Disulfide bridge between the Cys residues at
positions 2 and 7

<220>
<221> MOD_RES
<222> (37)
<223> amidated Tyr (Tyrosinamide)

<400> 28
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Thr Asn Phe Leu
1 5 10 15

Val Arg Ser Ser His Asn Leu Gly Pro Ala Leu Pro Pro Thr Asp Val
20 25 30

Gly Ser Asn Thr Tyr
35

<210> 29
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<221> MOD_RES
<222> (25)
<223> amidated Tyr (Tyrosinamide)

<400> 29
Val Leu Gly Lys Leu Ser Gln Glu Leu His Lys Leu Gln Thr Tyr Pro
1 5 10 15

Arg Thr Asn Thr Gly Ser Asn Thr Tyr
20 25

<210> 30
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<221> MOD_RES
<222> (25)
<223> amidated Pro (Prolinamide)

<400> 30
Val Leu Gly Lys Leu Ser Gln Glu Leu His Lys Leu Gln Thr Tyr Pro
1 5 10 15
Arg Thr Asn Thr Gly Ser Gly Thr Pro
20 25

<210> 31
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide construct

<220>
<221> MOD_RES
<222> (1)
<223> Lys, Ser, Ala, des-alpha-amino Lys, or acetylated
Lys

<220>
<221> MOD_RES
<222> (2)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (7)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (13)
<223> Ala, Ser, or Thr

<220>
<221> MOD_RES
<222> (17)
<223> Val, Leu, or Ile

<220>
<221> MOD_RES
<222> (18)
<223> His or Arg

<220>
<221> MOD_RES
<222> (19)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (20)
<223> Ser, Thr, Gln, or Asn

<220>
<221> MOD_RES
<222> (21)
<223> Asn, Gln, or His

<220>
<221> MOD_RES
<222> (23)
<223> Phe, Leu, or Tyr

<220>
<221> MOD_RES
<222> (25)
<223> Ala or Pro

<220>
<221> MOD_RES
<222> (26)
<223> Ile, Val, Ala, or Leu

<220>
<221> MOD_RES
<222> (28)
<223> Ser, Pro, Leu, Ile, or Thr

<220>
<221> MOD_RES
<222> (29)
<223> Ser, Pro, or Thr

<220>
<221> MOD_RES
<222> (31)
<223> Asn, Asp, or Gln

<400> 31
Xaa Xaa Asn Thr Ala Thr Xaa Ala Thr Gln Arg Leu Xaa Asn Phe Leu
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Asn Xaa Gly Xaa Xaa Leu Xaa Xaa Thr Xaa Val
20 25 30

Gly Ser Asn Thr Tyr
35